

GenCore version 5.1.4\_p5\_4578  
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OM nucleic - nucleic search, using sw model

Run on: March 26, 2003, 11:15:29 ; Search time 196.545 Seconds  
(without alignments)  
263.532 Million cell updates/sec

|                |                          |
|----------------|--------------------------|
| Title:         | US-10-086-184-1          |
| Perfect score: | 23                       |
| Sequence:      | 1 aatcgctcgcgagcggaac 23 |

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 2185239 reqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 2063506

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Minimum DB seq length: 0
Maximum DB seq length: 40
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : **\_N\_Genseq.010002.\***

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22: /SID52/gcgdata/genseq/genseqn-emb1/NA2001A.DAT.\*  
23: /SID52/gcgdata/genseq/genseqn-emb1/NA2001B.DAT.\*  
24: /SID52/gcgdata/genseq/genseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB | ID       | Description          |
|------------|-------|-------------|--------|----|----------|----------------------|
| 1          | 15    | 65.2        | 40     | 22 | AAD14572 | Arabidopsis thaliana |
| 2          | 15    | 65.2        | 40     | 22 | AA507877 | Binding site select  |
| 3          | 15    | 65.2        | 40     | 22 | AAD08945 | Arabidopsis thaliana |
| 4          | 15    | 65.2        | 40     | 22 | AA503391 | A group IA abscisic  |
| 5          | 15    | 65.2        | 40     | 22 | AA500410 | ABRE binding sequen  |
| 6          | 14.8  | 64.3        | 18     | 22 | AAH47535 | Human Her-3 mRNA     |
| c          | 14.6  | 63.5        | 31     | 20 | AA06374  | Human biallelic po   |
| c          | 8     | 14.2        | 38     | 21 | AA07745  | Single base exten    |
| c          | 9     | 13.8        | 60.0   | 23 | AA577135 | Nerve mutation fac   |

|   |    |      |      |    |    |           |                      |
|---|----|------|------|----|----|-----------|----------------------|
| C | 10 | 13.8 | 60.0 | 26 | 17 | AA08994   | Insulin response     |
| C | 11 | 13.8 | 60.0 | 29 | 18 | AA051155  | Homeoprotein regul   |
| C | 12 | 13.8 | 60.0 | 33 | 14 | AA0492828 | Degenerin PCR prim   |
| C | 13 | 13.8 | 60.0 | 37 | 17 | AA08992   | Degenerin PCR prim   |
| C | 14 | 13.6 | 59.1 | 29 | 15 | AA061760  | HEV strain BUR-121   |
| C | 15 | 13.6 | 59.1 | 29 | 17 | AA073471  | HEV strain Burma-1   |
| C | 16 | 13.6 | 59.1 | 29 | 19 | AA071681  | HEV ORF proteins e   |
| C | 17 | 13.6 | 59.1 | 34 | 19 | AA040446  | primer 2, used to    |
| C | 18 | 13.6 | 59.1 | 34 | 20 | AA079944  | PCR primer for EDD   |
| C | 19 | 13.4 | 58.3 | 15 | 21 | AA073137  | Forward primer #17   |
| C | 20 | 13.4 | 58.3 | 18 | 20 | AA032002  | MSH2 gene specific   |
| C | 21 | 13.4 | 58.3 | 26 | 22 | AA016181  | Soybean 240017 reg   |
| C | 22 | 13.4 | 58.3 | 33 | 15 | AA044662  | PCR primer for pcr   |
| C | 23 | 13.4 | 58.3 | 33 | 15 | AA044660  | PCR primer for amp   |
| C | 24 | 13.4 | 58.3 | 36 | 24 | ABA01674  | Human androgen rec   |
| C | 25 | 13.4 | 58.3 | 40 | 21 | AA073139  | Single base extens   |
| C | 26 | 13.2 | 57.4 | 24 | 21 | AA078589  | Rat hepatocyte cat   |
| C | 27 | 13.2 | 57.4 | 27 | 19 | AA043514  | Primer for mouse R   |
| C | 28 | 13.2 | 57.4 | 33 | 14 | AA049299  | Degenerin PCR prim   |
| C | 29 | 13   | 56.5 | 27 | 18 | AA068630  | Human fil1 VEGF re   |
| C | 30 | 13   | 56.5 | 28 | 18 | AA066979  | Human endothelial-   |
| C | 31 | 13   | 56.5 | 28 | 21 | AA028715  | Human EMAP III PCR   |
| C | 32 | 13   | 56.5 | 28 | 21 | AA028715  | Human EMAP III PCR   |
| C | 33 | 12.8 | 55.7 | 23 | 15 | AA066278  | PCR primer for amp   |
| C | 34 | 12.8 | 55.7 | 23 | 24 | AB015161  | Chimeric polymerase  |
| C | 35 | 12.8 | 55.7 | 23 | 24 | AB015161  | Chimeric polymerase  |
| C | 36 | 12.8 | 55.7 | 27 | 22 | AA099060  | Immunostimulatory    |
| C | 37 | 12.8 | 55.7 | 27 | 22 | AA099061  | Immunostimulatory    |
| C | 38 | 12.8 | 55.7 | 27 | 22 | AA099864  | Immunostimulatory    |
| C | 39 | 12.8 | 55.7 | 27 | 24 | AB018717  | Immunostimulatory    |
| C | 40 | 12.8 | 55.7 | 27 | 24 | AB019012  | Immunostimulatory    |
| C | 41 | 12.8 | 55.7 | 30 | 14 | AA049268  | cat-4 regulated. Syn |
| C | 42 | 12.8 | 55.7 | 30 | 24 | AB049489  | Fed regulated gene   |
| C | 43 | 12.6 | 54.8 | 30 | 22 | ABA02872  | Soybean coproporph   |
| C | 44 | 12.6 | 54.8 | 30 | 22 | AA046574  | Soybean coproporph   |
| C | 45 | 12.6 | 54.8 | 30 | 23 | AB019774  | Endogenous human G   |

## ALIGNMENTS

RESULT 1  
AAD14572  
ID AAD14572 standard; DNA; 40 BP.

AC AAD14572;

DT 01-NOV-2001 (first entry)

DE Arabidopsis thaliana ABF binding sequence #19.

KM Abscisic acid responsive element; ABRE; ABRE-binding factor; ABF;  
KM stress treatment; transgenic plant; environmental stress; ds.

05 *Arabidopsis thaliana*.

| FH  | Key | Location/Qualifiers |
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FT / \*tag= a

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FT      misc_feature      29
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| PA                       | (KOKU-)-KOREA KUMHO PETROCHEMICAL CO LTD.   |
| XX                       |   |
| PI                       | K1m SY;   |
| XX                       |   |
| DR                       | WPI, 2001-366358/38.  |
| XX                       |   |
| PT                       | New nucleic acid encoding abscisic acid responsive element binding factor 4, useful for generating transgenic plants, which are tolerant to multiple environmental stresses -   |
| XX                       |   |
| PS                       | Disclosure; Fig 5B; 42pp; English.  |
| XX                       |   |
| CC                       | The invention relates to nucleic acid encoding the abscisic acid responsive element (ABRE)-binding factor 4 (ABF4). ABF4 belongs to the ABF family of factors which bind abscisic acid responsive elements in plants. Expression of ABFs is inducible by abscisic acid and various stress treatments. ABFs have the potential to activate a large number of abscisic acid/stress responsive genes and thus a nucleic acid molecule encoding ABF4 is useful for generating transgenic plants that are tolerant to multiple environmental stresses. The present sequence is Arabidopsis thaliana ABF binding sequence which contains the group IA consensus sequence. |
| CC                       |   |
| XX                       | Sequence 40 BP; 9 A; 12 C; 12 G; 7 T; 0 other;  |
| SO                       |   |
| Query Match              | 65.2%; Score 15; DB 22; Length 40;  |
| Best Local Similarity    | 78.3%; Pred. No. 8e+02;   |
| Matches 18; Conservative | 0; Mismatches 5; Indels 0; Gaps 0;  |
| Oy                       | 1. AATCGCGCTCCGAGCGGGAAC 23<br>   |
| Db                       | 2. AATTCGCTCTAAGCGGAGAC 24  |
| RESULT 2                 |   |
| AA507877                 |   |
| ID                       | AA507877 standard; DNA; 40 BP.  |
| XX                       |   |
| AC                       | AA507877;   |
| XX                       |   |
| DT                       | 23-OCT-2001 (first entry)   |
| XX                       |   |
| DE                       | Binding site selection assay group IA sequence #19.   |
| XX                       |   |
| KW                       | Abscisic acid responsive element binding factor; ABF; bz1P; ss; G/ABRE; G-box-like ABRE; coupling element-like ABRE; C/ABRE; transgenic plant;  |
| KW                       | stress responsive gene; environmental stress; crees;  |
| XX                       | binding site selection assay.   |
| XX                       |   |
| OS                       | Synthetic.  |
| XX                       |   |
| PH                       | Key   |
| FT                       | misc_feature  |
| FT                       | Location/Qualifiers   |
| FT                       | 20..29  |
| FT                       | /*tag= B  |
| FT                       | /note= "Group IA consensus sequence"  |
| PN                       | EP1097999-A2.   |
| XX                       |   |
| PD                       | 09-MAY-2001.  |
| XX                       |   |
| PF                       | 29-JUN-2000; 2000EP-0305459.  |
| XX                       |   |
| PR                       | 04-NOV-1999; 99KR-0048477.  |
| XX                       |   |
| PA                       | (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.   |
| XX                       |   |
| PI                       | K1m SY;   |
| XX                       |   |
| DR                       | WPI; 2001-337113/36.  |
| XX                       |   |
| PT                       | Nucleic acid encoding novel transcription factors that bind to various abscisic acid responsive elements, for generating stress tolerant transgenic plants -  |
| PT                       |   |

|          |   |
|----------|---|
| PS       | Disclosure; Fig 5B; 37pp; English.  |
| XX       |   |
| CC       | The sequence represents an oligonucleotide studied in a binding site      |
| CC       | selection assay, for studying abscisic acid responsive element binding    |
| CC       | factor (ABF) proteins. The oligonucleotide contains the 1A consensus      |
| CC       | sequence. ABFs are bZIP class transcription factors that can bind to two  |
| CC       | classes of ABRE, namely G-box-like ABREs (G/ABRE) and coupling            |
| CC       | element-like ABREs (C/ABRE). Expression of ABF is inducible by abscisic   |
| CC       | acid and various stress treatments and they can transactivate an          |
| CC       | ABRE-containing reporter gene in yeast. Therefore, the ABFs are useful    |
| CC       | for activating a large number of abscisic acid or stress responsive genes |
| CC       | and for generating transgenic plants that are tolerant to multiple        |
| CC       | environmental stresses.   |
| XX       |   |
| SO       | Sequence 40 BP; 9 A; 12 C; 12 G; 7 T; 0 other;                            |
| XX       |   |
| QY       | Query Match 65.2%; Score 15; DB 22; Length 40;                            |
| DB       | Best Local Similarity 78.3%; Pred. No. 8e+02;                             |
|          | Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0                |
|          | 1 AATCGCCTCCGAGCGGGGAAC 23  |
|          | 2 AATCGCCTCTAAGCGGGACAC 24  |
| XX       |   |
| RESULT 3 |   |
| AD08945  |   |
| ID       | AD08945 standard; DNA; 40 BP.   |
| XX       |   |
| AC       | AD08945;  |
| XX       |   |
| DT       | 04-SEP-2001 (first entry)   |
| XX       |   |
| DE       | Arabidopsis thaliana ABF binding sequence #18.                            |
| XX       |   |
| KM       | Abscisic acid responsive element binding factor; ABF; ABRE;               |
| XX       | bZIP class transcription factor; transgenic plant; ds.                    |
| XX       |   |
| OS       | Arabidopsis thaliana.   |
| XX       |   |
| PH       | Key Location/Qualifiers   |
| FT       | misc_feature 19..29   |
| FT       | /*tag= a  |
| FT       | /note= "Conserved region"   |
| FT       | 29  |
| FT       | /*tag= b  |
| FT       | /note= "Base "S" is found at this location in the                         |
| FT       | sequence shown as SEQ ID NO: 51 in the sequence listing"                  |
| XX       |   |
| PN       | US6245905-B1.   |
| XX       |   |
| PD       | 12-JUN-2001.  |
| XX       |   |
| PF       | 14-SEP-2000; 2000US-0661569.  |
| XX       |   |
| PR       | 12-OCT-1999; 99US-0416050.  |
| XX       |   |
| PA       | (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.                                 |
| XX       |   |
| PI       | Kim SY;   |
| XX       |   |
| DR       | WPI; 2001-380516/40.  |
| XX       |   |
| PT       | New abscisic acid responsive element binding factor 2 useful for          |
| PT       | activating abscisic acid/stress responsive genes, and generating          |
| PT       | transgenic plants that are tolerant to multiple environmental stresses    |
| PT       | -   |
| XX       |   |
| PS       | Disclosure; Fig 5B; 42pp; English.  |
| XX       |   |
| CC       | The parent discloses novel abscisic acid (ABA) responsive element         |
| CC       | (ABRE) binding factors (ABFs). ABFs are basic leucine zipper (bZIP)       |

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CC class transcription factors that bind to both G-box-like ABREs (G/ABREs)
CC and coupling element like ABREs (C/ABREs). ABFs have the potential to
CC activate a large number of abscisic acid/stress responsive genes, and
CC are therefore used to generate transgenic plants that are tolerant to
CC multiple environmental stresses.
CC The present DNA sequence is Arabidopsis thaliana ABF binding sequence
CC which contains the group IA consensus sequence.
CC Note: This sequence is stated to be the same as that shown as
CC SEQ ID NO: 51 in the sequence listing of the specification. However
CC the sequences differ at position 29.
XX
SQ Sequence 40 BP, 9 A, 12 C, 12 G, 7 T, 0 other;
Query Match 65.2%; Score 15; DB 22; Length 40;
Best Local Similarity 78.3%; Pred. No. 8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AATCGGCTCCAGCGCGGAAC 23
DB 2 AATCGCCTCTAAGCGGACAC 24
RESULT 4
AAS03391
ID AAS03391 standard; DNA; 40 BP.
AC AAS03391;
XX
DT 29-AUG-2001 (first entry)
XX
DE A group IA abscisic acid response element (G/ABRE).
XX
KM Abscisic acid response element; G/ABRE; ABRE binding factor; ABF;
KM transgenic plant; stress responsive gene; environmental stress response;
KM probe; ds; G-box.
XX
OS Synthetic.
XX
XX Key ' Location/Qualifiers
FH protein_bind 19.27
FT /tag= a
FT /bound_molecy= "ABF"
XX
PN US6218527-B1.
XX
PD 17-APR-2001.
XX
PF 19-SEP-2000; 2000US-0664800.
XX
PR 12-OCT-1999; 99US-0416050.
XX
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI Kim SY;
XX
DR WPI: 2001-281059/29.
XX
PT Isolated nucleic acid molecule for generating environmental-stress
PT tolerant transgenic plants, encodes abscisic acid responsive
PT element-binding factor 3 -
XX
PS Disclosure; Column 43; 43pp; English.
XX
CC The sequence represents a group IA G-box containing abscisic acid
CC response element (G/ABRE), used in a gel mobility shift assay, testing
CC for the binding of ABRE binding factor, ABF1. The nucleic acid encoding
CC an ABF can be used to generate transgenic plants that are tolerant to
CC multiple environmental stresses e.g. drought, high salt, and cold/
CC freezing. Expression of the binding factor is inducible by abscisic acid
CC and various stress treatments, and can transactivate an abscisic acid
CC responsive element (ABRE)-containing a reporter gene in yeast. The
CC binding factor can activate a number of abscisic acid/stress responsive
CC genes.
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XX
SQ Sequence 40 BP, 9 A, 11 C, 12 G, 7 T, 1 other;
Query Match 65.2%; Score 15; DB 22; Length 40;
Best Local Similarity 78.3%; Pred. No. 8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AATCGGCTCCAGCGCGGAAC 23
DB 2 AATCGCCTCTAAGCGGACAC 24
RESULT 5
AAS00410
ID AAS00410 standard; CDNA; 40 BP.
AC AAS00410;
XX
DT 25-MAY-2001 (first entry)
XX
DE ABRE binding sequence 45, identified from binding site selection.
XX
KM Abscisic acid responsive element binding factor 1; ABF1; plant hormone;
KM drought; ABA-responsive element; ABRE; ABRE-binding factor; ABF;
KM basic leucine zipper; bZIP; G/ABRE; C/ABRE; transgenic plant;
KM environmental stress; ss.
XX
OS Arabidopsis thaliana.
XX
PN US6194559-B1.
XX
PD 27-FEB-2001.
XX
PR 12-OCT-1999; 99US-0416050.
XX
PR 12-OCT-1999; 99US-0416050.
XX
PA (KOKU-) KOREA KUMHO PETROCHEMICAL CO LTD.
XX
PI Kim SY;
XX
DR WPI: 2001-217937/22.
XX
PT New nucleic acid molecule encoding Abscisic acid responsive element
PT binding factor 1 (ABF1) which can be used to generate transgenic plants
PT that are tolerant to multiple environmental stresses -
XX
PS Disclosure; Fig 5B; 42pp; English.
XX
CC The sequence represents the ABRE binding sequence 45, identified from
CC binding site selection analysis of abscisic acid responsive element
CC binding factors (ABFs), isolated from an Arabidopsis cDNA library.
CC Abscisic acid (ABA) is a major plant hormone involved in response to
CC adverse environmental conditions such as drought, high salt and cold/
CC freezing. This response involves induced expression of various genes.
CC ABA-responsive elements (ABREs) are cis-regulatory elements that mediate
CC the ABA-modulated gene expression, and interact with a novel class of
CC ABRE-binding factors (ABFs). ABFs are basic leucine zipper (bZIP) class
CC transcription factors that bind to both G/ABREs and C/ABREs. ABFs have
CC the potential to activate a large number of ABA/stress responsive genes
CC and can be used to generate transgenic plants that are tolerant to
CC multiple environmental stresses.
XX
SQ Sequence 40 BP, 9 A, 11 C, 12 G, 7 T, 1 other;
Query Match 65.2%; Score 15; DB 22; Length 40;
Best Local Similarity 78.3%; Pred. No. 8e+02;
Matches 18; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AATCGGCTCCAGCGCGGAAC 23
DB 2 AATCGCCTCTAAGCGGACAC 24
```

## RESULT 6

AAH47535/c

ID AAH47535 standard; DNA; 18 BP.

XX AAH47535;

XX 30-NOV-2001 (first entry)

XX Human Her-3 mRNA inhibiting antisense oligo ISIS # 19550.

XX Her-3; epidermal growth factor; EGF; receptor/tyrosine kinase; human;

XX antiinflammatory; cytostatic; antibacterial; antisense; ss.

XX Synthetic.

XX Homo sapiens.

XX US6277640-B1.

XX 21-AUG-2001.

XX 31-JUL-2000; 2000US-0630706.

XX 31-JUL-2000; 2000US-0630706.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowser LM;

XX WPI; 2001-535134/59.

XX Antisense compounds capable of modulating expression of human Her-3,

XX member of epidermal growth factor family of receptor/tyrosine kinases,

XX useful for preventing or delaying infection, inflammation or tumor

XX formation -

XX Claim 1; Column 42; 49pp; English.

XX The invention provides antisense compounds capable of inhibiting the

XX expression of human Her-3, a member of epidermal growth factor (EGF)

XX family of receptor/tyrosine kinases. The antisense oligonucleotides are

XX useful for inhibiting the expression of Her-3 in cells or tissues. They

XX are commonly used as research reagents and in diagnostics for example, to

XX elucidate the function of particular genes. The antisense compounds are

XX also useful for distinguishing between functions of various members of a

XX biological pathway and for research use. They are also utilized for

XX diagnostics, therapeutics, prophylaxis and in kits. They are useful

XX prophylactically, e.g. to prevent or delay infection, inflammation or

XX tumor formation. Sequences AAH47532-47615 represent chimeric antisense

XX CC phosphorothioate oligonucleotides having 2'-MOE wings and a deoxy gap,

XX used for the inhibition of Her-3 mRNA expression.

XX Sequence 18 BP; 2 A; 8 C; 5 G; 3 T; 0 other;

XX Query Match 64.3%; Score 14.8; DB 22; Length 18;

XX Best Local Similarity 88.9%; Pred. No. 9.5e+02;

XX Matches 16; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

XX Db 6 GGCTCCGAGCGGGAAC 23

XX 18 GGCTCCGAGGTGGCAAC 1

## RESULT 7

AAH06374/c

ID AAH06374 standard; DNA; 31 BP.

XX AAH06374;

XX 31-MAR-1999 (first entry)

XX Human bi-allelic polymorphic DNA fragment SGC33319.

XX

XX Polymorphism; bi-allelic; paternity testing; forensic; genetic mapping;

XX phenotypic typing; medicament; disease; marker; human; ss.

XX Homo sapiens.

XX MO9658529-A2.

XX 30-DEC-1998.

XX 22-JUN-1998; 98WO-US12930.

XX 24-JUN-1997; 97US-0050594.

XX (AFFY-) AFFYMETRIX INC.

XX Berno A, Chee M, Fan J, Lipshutz RJ;

XX WPI; 1999-080963/07.

XX New nucleic acid segments containing polymorphic sites - used for,

XX e.g. detecting a disease phenotype, in forensics, paternity testing

XX or genetic mapping of phenotypic traits

XX Claim 1; Page 23; 61pp; English.

XX Sequences AAH06101-X06558 represent human DNA fragments which contain

XX bi-allelic polymorphic markers. The base occupying the polymorphic site

XX is indicated by the appropriate IUPAC-IUB ambiguity code. These

XX fragments can be used in a method for determining polymorphic forms in

XX an individual. The invention further provides computer-readable storage

XX medium for storing data for access by an application programme being

XX executed on a data processing system. Such a method comprises a data

XX structure stored in the computer-readable storage medium, the data

XX structure including information resident in a database used by the

XX application programme and including records, each record comprising

XX information identifying a polymorphism shown in the above sequences. The

XX products and methods can be used for analysing polymorphic sites in

XX individuals for testing for the presence of a disease phenotype or in

XX forensics, paternity testing or genetic mapping of phenotypic traits.

XX They can also be used for the production of polypeptides expressed by

XX variant genes and for the production of transgenic animals. The nucleic

XX acid segments can also be used in the manufacture of medicaments for the

XX treatment or prophylaxis of diseases.

XX Sequence 31 BP; 5 A; 8 C; 8 G; 9 T; 1 other;

XX Query Match 63.5%; Score 14.6; DB 20; Length 31;

XX Best Local Similarity 73.9%; Pred. No. 1.2e+03;

XX Matches 17; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

XX Db 1 AAATCGGCTCCGAGCGGGAAC 23

XX 30 ACATCGAGCTACGAGCTCGAATC 8

## RESULT 8

AACT3135/c

ID AACT3135 standard; DNA; 38 BP.

XX AACT3135;

XX 02-FEB-2001 (first entry)

XX Single base extension primer #16 used in multiplexing PCR/SBE assay.

XX Oligonucleotide array; genotyping; single base extension reaction; SBE;

XX PCR primer; polymorphic locus; single nucleotide polymorphism; ss.

XX Unidentified.

XX MO200058516-A2.

XX PN MO200058516-A2.

XX OS MO200058516-A2.

XX XX MO200058516-A2.

XX XX 05-OCT-2000.

```

XX 27-MAR-2000; 2000WO-US08069.
XX
XX 26-MAR-1999; 99US-0126473.
XX 23-JUN-1999; 99US-0140359.
XX
XX (WHEED ) WHITEHEAD INST BIOMEDICAL RES.
XX (AFPY-) APFYMETRIX INC.
XX
XX Fan J, Hirschhorn JN, Huang X, Kaplan P, Lander ES, Lockhart DJ;
XX Ryder T, Sklar P;
XX WPI; 2000-656171/63.
XX
XX Universal array of oligonucleotides tags attached to a solid substrate
XX along with locus-specific tagged oligonucleotides useful in genotyping
XX using single base extension reactions
XX
XX Example 7; Page 49; 83pp; English.
XX
XX The present invention relates to an oligonucleotide array comprising
XX oligonucleotide tags fixed to a solid substrate. The oligonucleotide
XX array is useful for genotyping a nucleic acid sample at one or more loci
XX via single base extension (SBE) reactions. A pair of primers is used to
XX amplify a polymorphic locus in a sample e.g. a single nucleotide
XX polymorphism (SNP). The amplified nucleic acid product is then used as a
XX template in a SBE reaction with an extension primer. The present sequence
XX is one such SBE reaction primer used in the method of the present
XX invention. The SBE reaction products are used to form the oligonucleotide
XX array.
XX
XX Sequence 38 BP; 7 A; 13 C; 10 G; 8 T; 0 other;
XX
XX Query Match 61.7%; Score 14.2; DB 21; Length 38;
XX Best Local Similarity 84.2%; Pred. No. 1.9e+03;
XX Matches 16; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
XX
XX 4 TCGGCTCCGAGCGGGA 22
XX |||||
XX 36 TCGGCTCCGAGCTGGA 18
XX
XX RESULT 9
XX AAX77145/C
XX ID AAX77145 standard; DNA; 23 BP.
XX
XX AAX77145;
XX
XX 03-AUG-1999 (first entry)
XX
XX Nerve mutation factor DNA amplifying primer.
XX
XX Nerve mutation factor; chromosome 10; glioma; tumour suppressor;
XX brain tumour; astrocytoma; gene therapy; human; mouse; PCR primer; ss.
XX
XX Synthetic.
XX
XX WO9925827-A1.
XX
XX 27-MAY-1999.
XX
XX 24-AUG-1998; 98WO-JP03737.
XX
XX 14-NOV-1997; 97JP-0313211.
XX
XX (SUME ) SUMITOMO ELECTRIC IND CO.
XX
XX Nakamura H, Nakata M, Saya H, Yoshida M;
XX
XX WPI; 1999-347474/29.
XX
XX Human gene on chromosome 10 homologous to Drosophila neuralized
XX gene, useful in the diagnosis and gene therapy of brain tumors
XX

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XX Examples; Page 24; 78pp; Japanese.
XX
XX The invention relates to a protein which is a nerve mutation factor and
XX is the expression product of a gene located on chromosome 10. The gene
XX is in a region frequently deleted in highly malignant gliomas. Sequences
XX (AAX77135 and AAX77136) encoding human and mouse nerve mutation factors
XX (AAY21558 and AAY21559) are provided. The protein is believed to have
XX tumour suppressor activity. Polynucleotide sequences and antibodies to
XX the protein are diagnostic reagents for highly malignant brain tumors
XX such as astrocytoma where chromosome 10 deletion commonly occurs. The
XX gene may also be used for gene therapy of such tumors.
XX
XX Sequence 23 BP; 2 A; 8 C; 8 G; 5 T; 0 other;
XX
XX Query Match 60.0%; Score 13.8; DB 20; Length 23;
XX Best Local Similarity 88.2%; Pred. No. 2.9e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX 1 AAATCGGCTCCGAGCG 17
XX |||||
XX 22 AAAGCGGCTCGAGCG 6
XX
XX RESULT 10
XX AAT08994/C
XX ID AAT08994 standard; DNA; 26 BP.
XX
XX AAT08994;
XX
XX 25-JUL-1996 (first entry)
XX
XX Insulin response element A minimal DNA binding element.
XX
XX Insulin response element A; IRE-A; E2F; liver IRE-A;
XX Rb-associated protein; RbAP-1; E2F-1; rapamycin; inhibition;
XX insulin-induced; expression; carbohydrate uptake;
XX triglyceride biosynthesis; treatment; prevention; obesity;
XX type II diabetes mellitus; insulin dependent tumours;
XX minimal DNA binding element; ss.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX FH 1..17
XX FT misc_feature
XX /tag= a
XX /note= "contact sequence"
XX
XX 1
XX FT misc_feature
XX /tag= b
XX /note= "contact point"
XX
XX 5
XX FT misc_feature
XX /tag= c
XX /note= "contact point"
XX
XX 6
XX FT misc_feature
XX /tag= d
XX /note= "contact point"
XX
XX 7
XX FT misc_feature
XX /tag= e
XX /note= "contact point"
XX
XX 9
XX FT misc_feature
XX /tag= f
XX /note= "contact point"
XX
XX 10
XX FT misc_feature
XX /tag= g
XX /note= "contact point"
XX
XX 12
XX FT misc_feature
XX /tag= h
XX /note= "contact point"
XX
XX 14
XX FT misc_feature
XX /tag= i
XX /note= "contact point"
XX
XX 17
XX FT misc_feature
XX /tag= j
XX

```

```

PT /note= "contact point"
XX
XX WO9531104-A1.
XX
XX 23-NOV-1995.
XX
XX 10-MAY-1995; 95WO-US05835.
XX
XX 13-MAY-1994; 94US-0242409.
XX
XX (GENO ) GEN HOSPITAL CORP.
XX
XX Alexander-Bridges MC, Zhao H;
XX
XX WPI, 1996-049292/05.
XX
XX Use of rapamycin to inhibit insulin-induced adiposis - for treating
XX insulin-induced obesity, weight gain and other conditions associated
XX with hyperinsulinemia
XX
XX Example; Page 27; 55pp; English.
XX
XX The present sequence is the insulin response element A (IRE-A)
XX minimal DNA binding element, which binds, with identical contact
XX sequence contact points, to liver IRP-A, and the cloned
XX Rb-associated protein RBP-1 (E2F-1). This information was used in
XX the development of the invention, i.e. rapamycin inhibition of
XX insulin-induced expression of carbohydrate uptake, and
XX triglyceride biosynthesis genes, useful in the treatment and
XX prevention of obesity, type II diabetes mellitus and insulin
XX dependent tumours, etc..
XX
XX Sequence 26 BP; 4 A; 10 C; 4 G; 8 T; 0 other;
SQ
XX
XX Query Match 60.0%; Score 13.8; DB 17; Length 26;
XX Best Local Similarity 88.2%; Pred. No. 2.9e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 GCCTCCGAGCGCGGAAA 22
XX 18 GCCTGAGAGCGCGGAAA 2
DB
XX
XX RESULT 11
XX AAT51155
XX ID AAT51155 strand; DNA; 29 BP.
XX
XX AAT51155;
AC
XX
XX 18-AUG-1997 (first entry)
DT
XX
XX Homeoprotein regulator of insulin gene expression primer GST-GGGS.
DE
XX
XX Antibody; diabetes; breast cancer; insulin dependent diabetes;
XX hypoglycaemia; hyperglycaemia; polymerase chain reaction; ss.
XX
XX Synthetic.
OS
XX
XX WO9636711-A2.
XX
XX 21-NOV-1996.
XX
XX 09-MAY-1996; 96WO-US06608.
XX
XX 09-MAY-1995; 95US-0437607.
XX
XX (SALK ) SALK INST.
XX (STRA-) STRANG CANCER PREVENTION CENT.
XX
XX Leonard JN, Montminy MR;
XX
XX WPI, 1997-012086/01.
XX

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PT New homeo:protein regulator of insulin gene expression - and related
PT DNA and antibodies, useful for detecting e.g diabetes or breast
PT cancer
XX
XX Examples; Page 44; 96pp; English.
XX
XX The present sequence is primer GST-GGGS used in the examples in order
XX to more fully illustrate the preferred embodiments of the invention.
XX The HoxB13 gene encodes a homeoprotein regulator of insulin gene
XX expression. The novel homeoprotein regulator of insulin gene
XX is a protein (or its active fragments, agonists and/or mimics) which
XX binds the FLAT element of an insulin gene promoter; which is modulated
XX by a Ca2+-dependent Cam kinase IV; and which is homologous to a sequence
XX encoded by a Hox gene complex. Detection of altered levels of the HoxB13
XX protein indicates a disease related to glucose homeostasis, particularly
XX (non-)insulin dependent diabetes, hypo- or hyper-glycaemia, or also
XX breast cancer. Antibodies are useful as reagents for immunoassays. The
XX protein and compounds that promote and inhibit its production or
XX activity or its specific binding partners, are useful for preventing or
XX treating the specified diseases, especially where insulin is also being
XX administered.
XX
XX Sequence 29 BP; 4 A; 9 C; 10 G; 6 T; 0 other;
SQ
XX
XX Query Match 60.0%; Score 13.8; DB 18; Length 29;
XX Best Local Similarity 88.2%; Pred. No. 3e+03;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 CGGCTCCGAGCGCGGAAA 21
XX 3 CGGATCCGAGCGCGCGTA 19
DB
XX
XX RESULT 12
XX AAQ49298
XX ID AAQ49298 strand; DNA; 33 BP.
XX
XX AAQ49298;
AC
XX
XX 28-APR-1994 (first entry)
DT
XX
XX Degenerin PCR primer.
DE
XX
XX Long-distance homology; evolution; nematode;
XX hybridisation; lower organism; structural homologue;
XX Alzheimer's disease; cell death gene; PCR; polymerase chain reaction;
XX ciona intestinalis; echinoderm; lamprey; puffer fish;
XX mammal; probe; ss.
XX
XX Synthetic.
OS
XX
XX WO9320237-A.
XX
XX 14-OCT-1993.
XX
XX 01-APR-1993; 93WO-US03102.
XX
XX 01-APR-1992; 92US-0861458.
XX
XX (CAMP-) CAMBRIDGE NEUROSCIENCE INC.
XX
XX Johnson CD, Marchionni MA;
XX
XX WPI, 1993-336943/42.
XX
XX Long-distance homology cloning of genes from lower organisms -
XX used to identify DNA that codes for evolutionary conserved
XX aminoacid sequences
XX
XX Disclosure; Fig 14; 188pp; English.
XX
XX The primers (AAQ49297-049348) and probes (AAQ49322-049348) are used to
XX isolate degenerin homologues from genomic DNA templates from three
XX

```

CC nematodes: *Caenorhabditis elegans*, *C. briggsae*, *Ascaris suum*.  
 CC The primers were based on area I and II amino acid sequences common  
 CC to the degenerate gene family members DEG-1 and MEC-4 from *C. elegans*.  
 XX

Sequence 33 BP; 6 A; 7 C; 9 G; 5 T; 6 other;

Query Match 60.0%; Score 13.8; DB 14; Length 33;  
 Best Local Similarity 65.2%; Pred. No. 3e+03;  
 Matches 15; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 1 AATCGGCTCCGAGCGCGGAAAC 23  
 DB 3 AATCGATCCGACNCGRAAY 25

RESULT 13  
 AAT08992/C  
 ID AAT08992 standard; DNA; 37 BP.

AC AAT08992;

DT 25-JUL-1996 (first entry)

DE Transfection analysis minimal binding motif.

XX Insulin response element A; IRE-A; E2F; liver IRP-A;  
 XX Rb-associated protein; RbAP-1; E2F-1; rapamycin; inhibition;  
 KW insulin-induced; expression; carbohydrate uptake;  
 KW triglyceride biosynthesis; treatment; prevention; obesity;  
 KW type II diabetes mellitus; insulin dependent tumours;  
 KW electrophoretic mobility shift assay; EMSA;  
 KW transfection analysis; minimal binding motif; ss.

XX Synthetic.

OS W09531104-A1.

XX 23-NOV-1995.

PD 10-MAY-1995; 95WO-US05835.

XX 13-MAY-1994; 94US-0242409.

XX (GEMO) GEN HOSPITAL CORP.

PA Alexander-Bridges MC, Zhao H;

XX WPI; 1996-049292/05.

DR Use of rapamycin to inhibit insulin-induced adiposis - for treating  
 PT insulin-induced obesity, weight gain and other conditions associated  
 PT with hyperinsulinemia

XX Example; Page 21; 55pp; English.

XX The present sequence is a transfection analysis minimal binding  
 CC motif, which was used in an electrophoretic mobility shift assay to  
 CC characterize insulin response element A (IRE-A) like and E2F like  
 CC binding activities. IRE-A normally binds, with identical contact  
 CC sequence contact points, to liver IRP-A, and the cloned  
 CC Rb-associated protein RbAP-1 (E2F-1). This information was used in  
 CC the development of the invention, i.e. rapamycin inhibition of  
 CC insulin-induced expression of carbohydrate uptake, and  
 CC triglyceride biosynthesis genes, useful in the treatment and  
 CC prevention of obesity, type II diabetes mellitus and insulin  
 CC dependent tumours, etc..

XX Sequence 37 BP; 8 A; 14 C; 5 G; 10 T; 0 other;

Query Match 60.0%; Score 13.8; DB 17; Length 37;  
 Best Local Similarity 88.2%; Pred. No. 3e+03;  
 Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GGCTCCGAGCGCGGAAA 22  
 DB 29 GGCTGAGAGCGCGGAAA 13

RESULT 14  
 AA061760  
 ID AA061760 standard; CDNA; 29 BP.

XX AA061760;

DT 21-OCT-1994 (first entry)

DE HEV strain BUR-121 primer R81.

XX Hepatitis E virus; HEV; strain SAR-55; open reading frame; ORF; PCR;  
 KW antibody; detection; diagnosis; primers; stool suspension; amplify;  
 KW polymerase chain reaction; primer; Burma; strain BUR-121; ss.

OS Synthetic.

XX W09406913-A.

XX 31-MAR-1994.

PD 17-SEP-1993; 93WO-US08849.

XX 18-SEP-1992; 92US-0947263.

XX (USSH) US SEC DEPT HEALTH.

PA Emerson SU, Purcell RH, Tearev SA;

XX WPI; 1994-118462/14.

DR Purified hepatitis E strain SAR-55 virus - used to develop prods.  
 PT for use in detection, diagnosis, vaccines and therapy of  
 PT hepatitis E virus infection

XX Example 1; Page 40; 114pp; English.

XX The sequences given in AA045198-200 and AA061687-777 are primers which  
 CC were used in the isolation and amplification of the genomic sequence  
 CC of the hepatitis E virus (HEV) strain SAR-55. These primers were  
 CC based on sequences derived from the SAR-55 strain and a strain from  
 CC Burma (BUR-121). The amplified sequence contains three open reading  
 CC frames (ORFs). The proteins encoded by this sequence can be used to  
 CC stimulate the production of protective antibodies upon injection into  
 CC a mammal that would serve to protect the mammal upon challenge with  
 CC wild type HEV. The proteins can be used for detection and diagnosis  
 CC of HEV infection. This cDNA was isolated from primates inoculated  
 CC with stool suspensions obtained from hepatitis E patients.

XX Sequence 29 BP; 6 A; 10 C; 9 G; 4 T; 0 other;

Query Match 59.1%; Score 13.6; DB 15; Length 29;  
 Best Local Similarity 80.0%; Pred. No. 3.7e+03;  
 Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 ATCGGCTCCGAGCGCGGAAA 22  
 DB 8 ATCGGCTCCGAGCGCGGAAA 27

RESULT 15

AA072471  
 ID AAT27471 standard; DNA; 29 BP.

XX AAT27471;

DT 27-NOV-1996 (first entry)

DE HEV strain Burma-121 derived reverse primer 81 (ORF-1).

```

XX Hepatitis E virus; HEV; SAR-55 strain; enteric transmission;
KW structural region; antigen; detection; antibody; vaccine;
KW immunisation; infection; primer; Burma-121;
KW polymerase chain reaction; PCR; ss.
XX
OS Synthetic.
XX
PN WO9610580-A2.
XX
PD 11-APR-1996.
XX
PF 03-OCT-1995; 95MO-US13102.
XX
PR 03-OCT-1994; 94US-0316765.
XX
PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX
PI Emerson SU, Purcell RH, Tsarev SA;
XX
DR WPI; 1996-209320/21.
XX
PT Isolated and purified hepatitis E virus strain SAR-55 DNA - encodes
PT antigenic protein useful in diagnosis, prophylaxis and treatment of
PT hepatitis E virus infection
XX
PS Example 1; Page 43; 121pp; English.
XX
CC The present sequence is a hepatitis E virus (HEV) strain Burma-121
CC derived primer, used in the isolation of the HEV strain SAR-55
CC cDNA. The HEV strain SAR-55 was implicated in an enterically
CC transmitted non-A, non-B hepatitis in Pakistan. The protein encoded
CC by the structural region of the virus (i.e. ORF-2), which is
CC capable of forming HEV like particles, is useful for the detection
CC of HEV antibodies (pref. IgG or IgM) in blood, plasma, sera,
CC cerebrospinal fluid, tissue, urine or pleural fluid. The protein,
CC and anti-HEV antibodies generated using the protein, can also be
CC used in vaccines for immunising an animal against HEV infection.
CC The protein is identified as a band of greater than 50 kD
CC following SDS-PAGE of cell lysates of insect cells infected with
CC a HEV ORF-2 contg. baculovirus, i.e. the claimed recombinant
CC expression vectors pPIC9-1779, -1780 and -1781.
XX
SO Sequence 29 BP; 6 A; 10 C; 9 G; 4 T; 0 other;
Query Match 59.1%; Score 13.6; DB 17; Length 29;
Best Local Similarity 80.0%; Pred. No. 3.7e+03;
Matches 16; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 ATCGGCTCCGAGCGCGGAAA 22
DB 8 ATCGGCTCCGAGCGGTCAA 27

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Search completed: March 26, 2003, 11:22:02  
 Job time : 197.545 secs